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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 11-30-07
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/626,879
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Mod 'I Small. Antigen RNA...
Inventors (please provide full names): J. Han et al

Earliest Priority Date: 7/25/03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

~~Please Search Seq ID No 1 + 2.~~
~~Size limit to 100 NTS.~~

Please Search Seq ID No 1 + 2.
Size limit to 40 NTS.

Please Include Interference Search.
Thanks

STAFF USE ONLY

Searcher: _____

Searcher Phone #: _____

Searcher Location: _____

Date Searcher Picked Up: _____

Date Completed: _____

Searcher Prep & Review Time: _____

Online Time: _____

Type of Search

____ NA Sequence (#)

____ AA Sequence (#)

____ Structure (#)

____ Bibliographic

____ Litigation

____ Fulltext

____ Other

Vendors and cost where applicable

____ STN _____ Dialog

____ Questel/Orbit _____ Lexis/Nexis

____ Westlaw _____ WWW/Internet

____ In-house sequence systems

____ Commercial _____ Oligomer _____ Score/Length
____ Interference _____ SPDI _____ Encode/Transl

____ Other (specify)

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SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 9/18/07
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Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Mod 'I Small interfering RNA i
Inventors (please provide full names): J. HAN et al.

Earliest Priority Date: 7/10/03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No: 9
Size limit to 50 NTS.

STAFF USE ONLY

Searcher: _____

Searcher Phone #: _____

Searcher Location: _____

Date Searcher Picked Up: _____

Date Completed: _____

Searcher Prep & Review Time: _____

Online Time: _____

Type of Search

_____ NA Sequence (#)

_____ AA Sequence (#)

_____ Structure (#)

_____ Bibliographic

_____ Litigation

_____ Fulltext

_____ Other

Vendors and cost where applicable

_____ STN _____ Dialog

_____ Questel/Orbit _____ Lexis/Nexis

_____ Westlaw _____ WWW/Internet

_____ In-house sequence systems

_____ Commercial _____ Oligomer _____ Score/Length
_____ Interference _____ SPDI _____ Encode/Transl
_____ Other (specify)

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 21, 2007, 14:21:44 ; Search time 441 Seconds
(without alignments)
6435.935 Million cell updates/sec

Title: US-10-626-879-9
Perfect score: 383
Sequence: 1 gccagccccgauggggc.....aaagaaaaaccaaacgaaac 383

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 5640290

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: ~~~~~~

4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C 1	48.4	12.6	50	4	AAC92382	Aac92382 Oligonucl
2	48	12.5	48	2	AAZ23541	Aaz23541 HCV DNA f
3	47	12.3	47	8	ABZ81791	Abz81791 HCV 5' UT
4	46.8	12.2	50	13	ADS34712	Ads34712 siRNA-9 P
5	45	11.7	45	13	ADR47301	Adr47301 Caenorhab
6	44.8	11.7	48	2	AAZ23542	Aaz23542 Human DNA
7	44.4	11.6	46	2	AAV54438	Aav54438 Nucleotid
8	44	11.5	44	3	AAA50912	Aaa50912 Nucleic a
9	43	11.2	47	12	ADP87770	Adp87770 Extended
10	42	11.0	42	2	AAV15321	Aav15321 Hepatitis
11	42	11.0	42	2	AAV15321	Aav15321 Hepatitis

11	42	11.0	42	2	AAX60959	Aax60959 Hepatitis
12	42	11.0	42	15	AEF39282	Aef39282 HCV 224 t
13	42	11.0	49	14	ADW28911	Adw28911 Wild type
C 14	41.4	10.8	45	2	AAT09177	Aat09177 Hepatitis
C 15	41.4	10.8	45	2	AAV20718	Aav20718 Hepatitis
C 16	41.4	10.8	45	2	AAV22770	Aav22770 Capture/A
C 17	41.4	10.8	45	6	ABK86839	Abk86839 Human imm
C 18	41.4	10.8	45	8	AAD56316	Aad56316 Hepatitis
C 19	41.4	10.8	45	12	ADQ74916	Adq74916 HCV.Captu
C 20	41.4	10.8	45	14	AEB17468	Aeb17468 HCV 5'UTR
C 21	41.4	10.8	45	14	AEB54512	Aeb54512 HCV detec
22	41	10.7	41	2	AAX37635	Aax37635 HCV detec
23	41	10.7	41	6	ABK52637	Abk52637 Minority
24	41	10.7	41	6	ABK52638	Abk52638 Minority
C 25	41	10.7	41	6	AAL40116	Aal40116 Pathogeni
26	40.4	10.5	49	14	ADW28990	Adw28990 Hepatitis
27	40.4	10.5	49	14	ADW28992	Adw28992 Hepatitis
28	40.4	10.5	49	14	ADW28994	Adw28994 Hepatitis
29	40.4	10.5	49	14	ADW28988	Adw28988 Hepatitis
C 30	40.2	10.5	45	2	AAQ32626	Aaq32626 HCV antig
31	40	10.4	40	2	AAQ32627	Aaq32627 HCV antig
32	40	10.4	40	2	AAV54434	Aav54434 Nucleotid
C 33	40	10.4	40	2	AAV54436	Aav54436 Nucleotid
34	40	10.4	40	3	AAA86970	Aaa86970 Probe for
35	40	10.4	40	3	AAA93199	Aaa93199 Hepatitis
36	40	10.4	40	10	ADC46967	Adc46967 Synthesis
37	40	10.4	40	12	ADP87774	Adp87774 TEX contr
38	40	10.4	40	12	ADP87786	Adp87786 TEX synth
39	39.4	10.3	41	11	ADM68241	Adm68241 Directed
40	39.4	10.3	41	12	ADP87819	Adp87819 HCV fragm
C 41	39	10.2	39	2	AAX37633	Aax37633 HCV detec
C 42	39	10.2	39	13	ADR82689	Adr82689 Peptide n
C 43	39	10.2	39	13	ADR82699	Adr82699 Peptide n
C 44	39	10.2	39	13	ADR82699	ADR82699 Peptide n

Adr82698 Peptide n
Adw28909 Wild type

c 44 39 10.2 39 13 ADR82698
45 38.8 10.1 49 14 ADW28909

ALIGNMENTS

RESULT 1
AAC92382/c
ID AAC92382 standard; DNA; 50 BP.
XX
AC AAC92382;
XX
DT 26-MAR-2001 (first entry)
XX
DE Oligonucleotide sequence SEQ ID NO:10.
XX
KW Amplification; analysis; RNA transcription; RNA polymerase; detection;
KW bacterium; virus; foodstuff; soil; environmental water; seawater;
KW house dust; ss.
XX
OS Synthetic.
XX
PN WO200075371-A1.
XX
PD 14-DEC-2000.
XX
PF 05-JUN-2000; 2000WO-JP003647.
XX
PR 04-JUN-1999; 99JP-00157653.
XX
PA (TOYJ) TOSOH CORP.
XX
DT

PI Ishizuka T, Ishiquro T, Saitoh J, Sakai T;

XX

DR WPI; 2001-061738/07.

XX

PT Potentiated method for amplification of nucleic acids for detection in
PT biological samples.

XX

PS Example 4; Page 40; 42pp; Japanese.

XX

[illegible]

XX

SQ Sequence 50 BP; 11 A; 14 C; 18 G; 7 T; 0 U; 0 Other;

Query Match

```
12.6%; Score 48.4; DB 4; Length 50;
```

Best Local Similarity 78.0%; Pred. No. 0.00018;

Matches	39;	Conservative	10;	Mismatches	1;	Indels	0;	Gaps	0;
---------	-----	--------------	-----	------------	----	--------	----	------	----

QV 83 CCAUGGCGUUAUGAUGAGUGUGCAGCCUCCAGACCCCCCUCGCCG 132

[illegible]

2

Db 50 CCATGGCGTTAGTATGAGTGTGTGTCAGCCCTCCAGACCCCCCTCCCGG 1

RESULT 2

AAZ23541

ID AAZ23541 standard; DNA; 48 BP.

XX

AC AAZ23541;

XX

DT 21-DEC-1999 (first entry)

XX

DE HCV DNA fragment 1.

XX

KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
KW cellular; yeast; fungal; primer; ss.

XX

OS Hepatitis C virus.

XX

PN DE19814828-A1.

XX

PD 07-OCT-1999.

XX

PF 02-APR-1998; 98DE-01014828.

XX

PR 02-APR-1998; 98DE-01014828.

XX

PA (HOFF) ROCHE DIAGNOSTICS GMBH.

XX

PI Kessler C, Haberhausen G, Batz H, Oerum H;

XX

DR WPI; 1999-552286/47.

XX

PT Nucleic acid amplification assay for detecting viral, bacterial,
cellular yeast or fungal nucleic acids

DE HCV 5' UTR molecular interaction site 7 polynucleotide 2.
 XX
 KW HCV; 5' untranslated region; 5' UTR; molecular interaction;
 KW secondary structure; combinatorial library; screening; virucide; ss.
 XX
 OS Hepatitis c virus.
 XX
 FH Key Location/Qualifiers
 FT misc_binding 1. .4
 FT /*tag= a
 FT /bound_moiety= "Polynucleotide 1"
 FT /note= "forms double-stranded region with bases 14-17 of
 FT sequence in ABZ81790"
 FT misc_structure 5
 FT /*tag= b
 FT /note= "forms internal loop with base 13 of sequence in
 FT ABZ81790"
 FT misc_binding 6. .7
 FT /*tag= c
 FT /bound_moiety= "Polynucleotide 1"
 FT /note= "forms double-stranded region with bases 11-12 of
 FT sequence in ABZ81790"
 FT stem_loop 8. .19
 FT /*tag= d
 FT misc_binding 20. .21
 FT /*tag= e
 FT /bound_moiety= "Bases 30-31"
 FT /note= "forms double-stranded stem region with bases 30-
 FT 31"
 FT misc_structure 22. .29
 FT /*tag= f
 FT /note= "internal loop"
 FT misc_binding 23. .28
 FT /++++~
 FT

FT /*tag= g
 FT /bound_moiety= "Bases 42-47"
 FT /note= "forms double-stranded dangling structure"
 FT 30. .31
 FT /*tag= h
 FT /bound_moiety= "Bases 20-21"
 FT /note= "forms double-stranded stem region with bases 20-
 FT 21"
 FT 32. .40
 FT /*tag= i
 FT /bound_moiety= "Polynucleotide 1"
 FT /note= "forms double-stranded region with bases 2-10 of
 FT sequence in ABZ81790"
 FT 42. .47
 FT /*tag= g
 FT /bound_moiety= "Bases 23-28"
 FT /note= "forms double-stranded dangling structure"
 XX
 PN WO2003018747-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 19-AUG-2002; 2002WO-US026219.
 XX
 PR 22-AUG-2001; 2001US-0314236P.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Ecker DJ;
 XX
 DR WPI; 2003-300721/29.
 XX
 PT Polynucleotides useful for screening combinatorial libraries of compounds
 nm that inhibit or stimulate viral replication

PT that inhibit or stimulate viral replication, comprise molecular
 PT interaction sites of hepatitis C virus RNA having a defined secondary
 PT structure.
 XX
 PS Claim 26; Page 38; 63pp; English.
 XX
 CC The present sequence is that of the second polynucleotide of a molecular
 CC interaction site (number 7) that has been identified in the 5'
 CC untranslated region (5' UTR) of hepatitis C virus (HCV) RNA (see
 CC ABZ81793). The first polynucleotide forming site 7 is given in ABZ81790.
 CC The 2 polynucleotides together form a double-stranded RNA including
 CC internal and terminal loops and 2 dangling structures. The 8 molecular
 CC interaction sites identified in the HCV 5' UTR each have a secondary
 CC structure capable of interacting with cellular components, such as
 CC factors and proteins required for translation and other cellular
 CC processes. Nucleic acid molecules, polynucleotides or oligonucleotides
 CC comprising the molecular interaction sites can be used to screen,
 CC virtually or actually, combinatorial libraries of compounds that bind to
 CC them. Such compounds can be used to modulate the activity of HCV RNA and
 CC hence to modulate (inhibit or stimulate) viral replication. Thus, novel
 CC drugs, and agricultural and industrial chemicals, that operate through
 CC the modulation of HCV RNA can be identified
 XX
 SQ Sequence 47 BP; 6 A; 11 C; 18 G; 0 T; 12 U; 0 Other;

 Query Match 12.3%; Score 47; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 284 UGGUACUGCCUGAUGGGUGCUUGCGAGUGCCCCGGAGGUCUCGUA 330
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1 UGGUACUGCCUGAUGGGUGCUUGCGAGUGCCCCGGAGGUCUCGUA 47

RESULT 4

ADS34712

ID ADS34712 standard; DNA; 50 BP.

XX

AC ADS34712;

XX

DT 02-DEC-2004 (first entry)

XX

DE siRNA-9 PCR product, seq id 55.

XX

KW Virucide; antiinflammatory; hepatotropic; hepatitis C virus; HCV;
KW proliferation; siRNA; short interfering RNA; RNA interference;
KW gene silencing; ds.

XX

OS Unidentified.

XX

PN WO2004078974-A1.

XX

PD 16-SEP-2004.

XX

PF 23-JAN-2004; 2004WO-JP000605.

XX

PR 24-JAN-2003; 2003JP-00016750.

XX

PA (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.

PA (CHUS) CHUGAI SEIYAKU KK.

XX

PI Kohara M, Watanabe T, Taira K, Miyagishi M, Sudo M;

XX

DR WPI; 2004-662428/64.

XX

PT New oligo ribonucleotide or peptide nucleic acid capable of sequence-

DE

specifically binding with DNA of hepatitis C virus useful for inhibition

DT	18-NOV-2004	(first entry)
XX		
DE	Caenorhabditis elegans	holocentric protein (HCP) oligo, RNA-HCP (X-Y-Z).
XX		
KW	self assembling oligonucleotide;	binding target RNA; gene detection; ss.
XX		
OS	Caenorhabditis elegans.	
OS	Synthetic.	
XX		
PN	JP2004242585-A.	
XX		
PD	02-SEP-2004.	
XX		
PF	14-FEB-2003;	2003JP-00036013.
XX		
PR	14-FEB-2003;	2003JP-00036013.
XX		
PA	(SANK-) SANKO JUNYAKU CO LTD.	
XX		
DR	WPI;	2004-629600/61.
XX		
PT	Self assembling oligonucleotides,	by using splicing probe having region
PT	for binding target RNA,	splicing target RNA using ribonuclease,
PT	synthesizing RNA fragment with	required region of target RNA for self-
PT	assembling oligonucleotides.	
XX		
PS	Example;	SEQ ID NO 5; 27pp; Japanese.
XX		
CC	The invention relates to a novel method	for self assembling
CC	oligonucleotides. The method comprises:	using a splicing probe, which
CC	comprises a region for binding target RNA;	splicing the target RNA bound
CC	to the probe using a ribonuclease;	synthesising an RNA fragment
CC	containing a required region of the target RNA,	and self-assembling the
CC	oligonucleotides using the above obtained RNA fragment	the invention

oligonucleotides using the above obtained RNA fragment. The invention further comprises self-assembled oligonucleotides, obtained by the above method. The method is useful for self-assembling oligonucleotides. The method is useful for detecting a gene, which involves carrying out the method, and detecting the target DNA by detecting the self-assembled oligonucleotides. The method is efficient and requires no special machine and special reagents. The method also provides a low-cost and convenient gene detection method, without using a machine and is uncomplicated. This polynucleotide sequence represents an oligonucleotide used in the exemplification of the invention.

XX
SQ Sequence 45 BP; 10 A; 11 C; 14 G; 0 T; 10 U; 0 Other; 0

Query Match	11.7%;	Score 45;	DB 13;	Length 45;
Best Local Similarity	77.8%;	Pred. No. 0.0019;		
Matches 35;	Conservative 10;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 171 GAAUUGCCAGGACGACCGGGUCCUUUCUUGGAUCAACCCGCUCAA 215
 |||::||| ||| ||| ||| ||| ||| ::||| ::||| ::||| ::|||
 Db 45 GAATTGCCAGGACGACCGGGTCCTTTCTTGGATCAACCCGCTCAA 1

RESULT 6
AAZ23542
ID AAZ23542 standard; DNA; 48 BP.
XX
AC AAZ23542;
XX
DT 21-DEC-1999 (first entry)
XX
DE Human DNA fragment 1.
XX
KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;

KW	cellular; yeast; fungal; primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	DE19814828-A1.
XX	
PD	07-OCT-1999.
XX	
PF	02-APR-1998; 98DE-01014828.
XX	
PR	02-APR-1998; 98DE-01014828.
XX	
PA	(HOFF) ROCHE DIAGNOSTICS GMBH.
XX	
PI	Kessler C, Haberhausen G, Batz H, Oerum H;
XX	
DR	WPI; 1999-552286/47.
XX	
PT	Nucleic acid amplification assay for detecting viral, bacterial,
PT	cellular, yeast or fungal nucleic acids.
XX	
PS	Disclosure; Fig 4; 28pp; German.
XX	
CC	This invention describes a novel assay for a nucleic acid comprises: (a)
CC	generating amplification products from a fragment of the nucleic acid,
CC	(b) contacting the amplification products with a probe; and (c) detecting
CC	hybridization between the amplification product and the probe. The assay
CC	is useful for detection of viral, bacterial, cellular, yeast or fungal
CC	nucleic acids in human, animal, bacterial, plant, yeast or fungal
CC	samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell
CC	or liquid biopsy samples. This sequence represents a fragment of the
CC	human genome which is used in the method of the invention

[illegible]

PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA (SRLS-) SRL KK.
XX
DR WPI; 1998-560731/48.
XX
PT Determination of hepatitis C virus (HCV) gene - with real time detective
PT PCR and primer and probe used for determination.
XX
PS Claim 5; Page 6; 7pp; Japanese.
XX
CC This is the nucleotide sequence of a Hepatitis C virus (HCV) probe, used
CC in the method of the invention. This is a useful for the detection of the
CC HCV gene
XX
SQ Sequence 46 BP; 10 A; 11 C; 14 G; 11 T; 0 U; 0 Other;

Query Match 11.6%; Score 44.4; DB 2; Length 46;
Best Local Similarity 73.9%; Pred. No. 0.0028;
Matches 34; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 74 AGCGUCUAGCCCAUGGCGGUAGUAUGAGUGUGCAGCCUCCAGGA 119
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 AGCGTCTAGCCCATGGCGTTAGTATGAGTGTCGTGCAACCTCCAGGA 46

RESULT 8
AAA50912
ID AAA50912 standard; DNA; 44 BP.
XX
AC AAA50912;
XX
DT 17-OCT-2000 (first entry)
XX
DE Multiple acid target sequence for use with tunable internal dials

DE Nucleic acid target sequence for use with trackable optical disks.
XX
KW Probe; trackable optical disk; analyte-specific assay;
KW nucleic acid hybridisation; ss.
XX
OS Synthetic.
XX
PN WO200026677-A1.
XX
PD 11-MAY-2000.
XX
PF 26-OCT-1999; 99WO-US025136.
XX
PR 30-OCT-1998; 98US-00183842.
PR 14-MAY-1999; 99US-00311329.
PR 14-MAY-1999; 99US-0134368P.
XX
PA (BURS-) BURSTEIN LAB INC.
XX
PI Worthington MO, Virtanen J;
XX
DR WPI; 2000-399370/34.
XX
PT Trackable optical disc for confocal laser microscopy has information
PT layer with trackable structure and non-operational structure(s) which all
PT are concurrently readable by single optical pickup.
XX
PS Example 7; Page 90; 154pp; English.
XX
CC A trackable optical disc composed of an information layer with a
CC trackable structure and non-operational structure has been developed for
CC use in confocal laser microscopy. This disc can be used in a nucleic acid
CC -based analyte-specific assay, where specific adherence of a magnetic
CC bead to the disc surface is determined by nucleic acid hybridisation. The

OS Hepatitis C virus.

XX

FH Key Location/Qualifiers

FT misc_feature 1. .47

FT /*tag= a

FT /note= "All n are deoxyuridine".

XX

PN US2004115643-A1.

XX

PD 17-JUN-2004.

XX

PF 12-DEC-2002; 2002US-00318416.

XX

PR 12-DEC-2002; 2002US-00318416.

XX

PA (LIZA/) LIZARDI P M.

PA (GRIB/) GRIBANOV O G.

XX

PI Lizardi PM, Gribanov OG;

XX

DR WPI; 2004-468050/44.

XX

PT Amplifying nucleic acid for detecting nucleic acid, by extension of one

PT or more primers using target templates having replication terminating

PT feature, dissociation of primer from templates to produce multiple

PT extended primers.

XX

PS Disclosure; SEQ ID NO 2; 75pp; English.

XX

CC The invention relates to amplifying (M1) a nucleic acid, involving

CC contacting one or more extension primers (EP) and target templates (TT)

CC and incubating under conditions to promote interaction of (EP) and

CC templates, extension of (EP) using the interacting (TT), and dissociation

CC of the extended (EP) from (TT) to produce multiple (EP) from at

RESULT 10

AAV15321

ID AAV15321 standard; DNA; 42 BP.

XX

AC AAV15321;

XX

DT 25-MAR-2003 (revised)

DT 28-MAY-1998 (first entry)

XX

DE Hepatitis C virus probe 3 CH.

XX

KW Hepatitis C virus; HCV; PCR; detection; reverse transcription; probe;
KW enzyme immunoassay; viral RNA; ss.

XX

OS Synthetic.

OS Hepatitis C virus.

XX

PN WO9746716-A1.

XX

PD 11-DEC-1997.

XX

PF 03-JUN-1997; 97WO-IT000128.

XX

PR 07-JUN-1996; 96IT-RM000404.

XX

PA (WESA) WABCO BV.

XX

PI Bosio P, Strumia C, Clemenza F;

XX

DR WPI; 1998-042222/04.

XX

DE Hepatitis C virus; reverse transcription; probe; ss.

PT Detection of hepatitis C virus - by reverse transcription, single-step
PT PCR and detection by DNA enzyme immunoassay.
XX
PS Disclosure; Page 4; 26pp; English.
XX
CC The present sequence represents a probe involved in the method of the
CC present invention for detecting hepatitis C virus (HCV). The method
CC comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the
CC resulting cDNA by a single polymerase chain reaction in a reaction
CC mixture having a Mg2+/Taq polymerase ratio of about 100 nmole/enzyme unit
CC ; and (c) detecting the amplification product by DEIA (DNA enzyme
CC immunoassay) using an oligonucleotide probe. The sensitivity of this
CC method is at least equal to that achievable by more complicated assays
CC using nested PCR. (Updated on 25-MAR-2003 to correct PR field.)
XX

SQ Sequence 42 BP; 8 A; 12 C; 13 G; 9 T; 0 U; 0 Other;

Query Match 11.0%; Score 42; DB 2; Length 42;
Best Local Similarity 78.6%; Pred. No. 0.015;
Matches 33; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 157 CGGUGAGUACACCGGAUUGCCAGGACGACCGGGUCCUUUCU 198
Db 1 CGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTCT 42

RESULT 11
AAX60959
ID AAX60959 standard; DNA; 42 BP.
XX
AC AAX60959;
XX
DT 16-AUG-1999 (first entry)
vv

Seq Alignment

Please Scan + mail

ESULT 33

AAT05222/c

ID AAT05222 standard; DNA; 28 BP.

XX

AC AAT05222;

XX

DT 13-JUN-1996 (first entry)

XX

DE Hepatitis C virus antisense oligonucleotide A312.

XX

KW Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;

KW translation; in vivo; ex vivo; in vitro; treatment; prevention;

KW infection; antisense; non coding; region; NCR; core region; ss.

XX

OS Synthetic.

XX

PN WO9530746-A1.

XX

PD 16-NOV-1995.

XX

PF 08-MAY-1995; 95WO-US005812.

XX

PR 10-MAY-1994; 94US-00240382.

XX

PA (GEHO) GEN HOSPITAL CORP.

XX

PI Wakita T, Wands JR;

XX

DR WPI; 1995-404113/51.

XX

PT New anti:sense hepatitis C virus oligo:nucleotide(s) - used for

PT inhibiting HCV RNA translation, for the treatment or prevention of HCV

PT infection.

XX

PS Claim 1; Page 29; 50pp; English.

XX

CC The present oligonucleotide (ON) inhibits the expression of hepatitis C

CC virus (HCV) RNA, specifically HCV type II and type III protein synthesis

CC is inhibited by 45% and 18%, respectively. The ONs of the invention

CC inhibit translation of HCV types I-V RNA in vivo, ex vivo or in vitro,

CC and can therefore be used to treat or prevent HCV infection. The

CC antisense ONs comprise 10-28 nucleotides complementary to the entire HCV

CC 5'-non-coding and part of the core region. The A or S in the ONs name

CC denotes antisense or sense, and the no. indicates the position of the 5'-

CC end of the ON. The ON was tested at 10 fold molar excess to HCV RNA

XX

SQ Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 28;

Best Local Similarity 66.7%; Pred. No. 1.3;

Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUACUGCCUGAUAGGGUGCUU 21

|:|:|:|:|:|:|:|:|:|:

Db 27 GTACTGCCTGATAGGGTGCTT 7

ESULT 27

AR094974/c

LOCUS AR094974 28 bp DNA linear PAT 08-SEP-2000

DEFINITION Sequence 12 from patent US 6001990.

ACCESSION AR094974

VERSION AR094974.1 GI:10022401

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 28)

AUTHORS Wands,J.R., Wakita,T. and Moradpour,D.

TITLE Antisense inhibition of hepatitis C virus

JOURNAL Patent: US 6001990-A 12 14-DEC-1999;

FEATURES Location/Qualifiers

source 1..28

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 28;

Best Local Similarity 66.7%; Pred. No. 85;

Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUACUGCCUGAUAGGGUGCUU 21

|:|:|:|:|:|:|:|:

Db 27 GTACTGCCTGATAGGGTGCTT 7

RESULT 36

AAZ57757/c

ID AAZ57757 standard; DNA; 28 BP.

XX

AC AAZ57757;

XX

DT 05-APR-2000 (first entry)

XX

DE Hepatitis C virus antisense inhibitor oligonucleotide A312.

XX

KW Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;

KW anti-inflammatory; translation inhibition; HCV infection; virucide.

XX

OS Hepatitis C virus.

XX

PN US6001990-A.

XX

PD 14-DEC-1999.

XX

PF 07-JUN-1995; 95US-00474700.

XX

PR 10-MAY-1994; 94US-00240382.

XX

PA (GEHO) GEN HOSPITAL CORP.

XX

PI Moradpour D, Wands JR, Wakita T;

XX

DR WPI; 2000-104900/09.

XX

PT Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating

PT Hepatitis C virus infections.

XX

PS Claim 1; Col 23; 31pp; English.

XX

CC This sequence is an antisense oligonucleotide that hybridises to
CC Hepatitis C virus (HCV) RNA, under physiological conditions. The
CC invention relates to HCV antisense oligonucleotides, and also for a
CC vector comprising a nucleotide sequence which is transcribed in an animal
CC cell to generate an antisense oligonucleotide. The oligonucleotides have
CC virucide, hepatotropic and anti-inflammatory activity, and are useful for
CC treating HCV infection by inhibiting translation of type I-V HCV RNA.
CC Hepatitis C virus is a positive strand RNA virus, and is the major
CC causative agent of post-transfusion hepatitis. Persistent HCV infection
CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma

XX

SQ Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 3; Length 28;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUACUGCCUGAUAGGGUGCUU 21
|:|:|:|:|:|:|:|:
Db 27 GTACTGCCTGATAGGGTGCTT 7

XX Hepatitis C virus (HCV) positive control primer.

DE

XX

KW Nucleic acid detection; pathogen; bacteria; virus; hepatitis C virus;

KW HCV; hepatitis B; HBV; hepatitis G; HGV; HIV; fungus; protozoa; ss;

KW parasite; mycoplasma; genetic mutation; food contamination; PCR primer.

XX

OS Synthetic.

OS Hepatitis C virus.

XX

PN WO9928503-A1.

XX

PD 10-JUN-1999.

XX

PF 16-NOV-1998; 98WO-US024494.

XX

PR 03-DEC-1997; 97IT-RM000749.

XX

PA (DIAS-) DIASORIN INT INC.

XX

PI Primi D, Mantero G;

XX

DR WPI; 1999-371139/31.

XX

PT Detection of single-stranded polynucleotide analytes.

XX

PS Example 12; Page 68; 73pp; English.

XX

CC The invention relates to a new method for detection of single-stranded

CC (ss) polynucleotide analytes that comprises using ss polynucleotide

CC probes which hybridize to the analyte and are bound to a solid support

CC where double-stranded (ds) polynucleotides are detected. The method can

CC be used for detecting ss PN analytes for the detection of pathogens such

CC as bacteria, viruses such as hepatitis C (HCV), hepatitis B (HBV)

as bacteria, viruses such as hepatitis C (HCV), hepatitis B (HBV), hepatitis G (HGV), or HIV, fungi, protozoa, parasites or mycoplasma. The method can be used to detect the presence of genetic mutations which have diagnostic or prognostic value. Pathogen contamination of food and drink supplies can also be detected using the method. The method provides for the sensitive and specific detection of ss PN analytes at concentration as low as 0.1fg

XX
SQ Sequence 42 BP; 8 A; 12 C; 13 G; 9 T; 0 U; 0 Other; 0

Query Match	11.0%;	-Score 42;	DB 2;	Length 42;
Best Local Similarity	78.6%;	Pred. No.	0.015;	

Matches	33;	Conservative	9;	Mismatches	0;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

QY 157 CGGUGAGUACACCGGAUUGCCAGGACGACCGGGUCCUUUCU 198

Db 1 CGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTCT

RESULT 12

AEF39282

ID AEF39282 standard; DNA; 42 BP.

XX

AC AEF39282;

XX

DT 23-MAR-2006 (first entry)

XX

DE HCV 224 targeted DNA fragment SEQ ID NO 40.

XX

ds; enzyme engineering; DNA cleavage; ribonuclease; ribozyme delta;
KW RNA cleavage.

XX

OS Hepatitis C virus.

VV

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PN
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PD
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XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC

WO2006002547-A1.

12-JAN-2006.

06-JUL-2005; 2005WO-CA001051.

06-JUL-2004; 2004US-0585093P.

(UYSH) UNIV SHERBROOKE.

Perreault J, Bergeron L;

WPI; 2006-090285/09.

New target-dependent nucleic acid adapter comprising a blocker stem sequence or a biosensor sequence, useful for improving specificity of a nucleic acid sequence for a target sequence.

Disclosure; SEQ ID NO 40; 145pp; English.

This invention describes a novel target-dependent nucleic acid adapter, to be matched to a substrate comprising a target sequence, has a nucleic acid sequence comprising: a blocker stem sequence complementary to a portion of the sequence and a biosensor sequence having a sequence complementary to the target sequence and improving the specificity of the sequence for the target sequence. In the absence of the target sequence of the substrate, the blocker stem sequence forms an intramolecular stem with the nucleic acid sequence linked to it, preventing exposition of the nucleic acid sequence; thus locking the nucleic acid sequence of the adapter in an inactive conformation. In the presence of target sequence of the substrate, the biosensor sequence forms conventional Watson-Crick base pairs with the target sequence and the blocker stem sequence dissociates from the intramolecular stem, thus exposing the nucleic acid

04-JUL-2003; 2003EP-00291676.

(INSP) INST PASTEUR.
(INSP) INST PASTEUR HELLENIQUE.

Mavromara P, Niki V;

WPI; 2005-067632/08.
P-PSDB; ADW28912.

Novel shorter form core+1 protein of hepatitis C virus, useful for in vitro method for detection of infection by HCV or for preparing immunogenic composition against HCV infection.

Disclosure; SEQ ID NO 25; 80pp; English.

This invention relates to a novel Hepatitis C virus (HCV) core+1 protein that can be used to elicit a CTL response against HCV infection. Specifically, it refers to a truncated form of the core+1 protein that is the product of translation of a coding sequence that consists of all or a portion of the nucleotide sequence extending from nucleotide 598-920 within the core+1 open reading frame (ORF) of HCV. The present invention describes engineered mutations designed to introduce premature stop codons and hence generate various truncated core+1 HCV proteins that can be used for preparing immunogenic compositions against HCV infection i.e. as antigens for the production of HCV antibodies. Accordingly, it provides an in vitro method useful for the detection of HCV infection that involves determining the presence of these antibodies, in particular antigen-antibody complexes can be detected by immunoassay (direct detection) or ELISA (indirect detection). Furthermore, it refers to a screening method to identify virucidal compounds that interact with viral propagation in cells infected by HCV, such that successful compounds can be used in the preparation of a medicine for the treatment of disorders induced by or associated with HCV infection.

CC induced by or associated with HCV infection. This oligonucleotide
CC sequence is a wild type HCV type 1a core+1 DNA fragment of the invention.

XX
SQ Sequence 49 BP; 24 A; 15 C; 5 G; 5 T; 0 U; 0 Other;

Query Match	11.0%;	Score 42;	DB 14;	Length 49;
Best Local Similarity	88.1%;	Pred. No. 0.015;		
Matches 37; Conservative	5;	Mismatches 0;	Indels 0;	Gaps 0;

QY
342 AUGAGCACGAAUCCUAAAACCUCAAAGAAAAACC CAAACGUAAC 383

Dbl
1 ATGAGCACGGAATCCTAAACCTCAAAGAAAAACC CAAACGTAAC 42

RESULT 14	
AAT09177/c	
ID	AAT09177 standard; DNA; 45 BP.
XX	
AC	AAT09177;
XX	
DT	21-OCT-2004 (revised)
DT	14-AUG-1996 (first entry)
XX	
DE	Hepatitis C virus specific capture/amp-probe-1A (HCV A).
XX	
KW	Ligase dependent polymerase chain reaction; LD-PCR; probe; hybridisation;
KW	ligand binding pair; ligase; paramagnetic bead; primer; amplification;
KW	hepatitis; untranslated region; UTR; rRNA; ss.

OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FTT		/++++-

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FH	Key	Location/Qualifiers
FT	misc_binding	5. .45
FT		/+--+--

FT /*tag= a
FT /bound_moiety
FT /note= "complementary to Hepatitis C virus 5'
FT untranslated region"
XX
PN WO9535390-A1.
XX
PD 28-DEC-1995.
XX
PF 14-JUN-1995; 95WO-US007671.
XX
PR 22-JUN-1994; 94US-00263937.
XX
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Zhang DY;
XX
DR WPI; 1996-058427/06.
XX
PT Ligation dependent polymerase chain reaction - for the detection of
PT infectious pathogens and abnormal human genes, e.g. HIV and neoplasia.
XX
PS Claim 47; Page 53; 100pp; English.
XX
CC A novel method of detecting a target nucleic acid (TNA) sequence involves
CC use of the ligase dependent polymerase chain reaction method (LD-PCR). In
CC this method, two probes are provided. The first probe contains a region
CC at the 5' end which is complementary and will hybridise with the TNA, the
CC 3' end of the first probe is generic and is bound to one half of a ligand
CC binding pair (LBP). The second probe contains a region at the 5' end
CC which is complementary to a region in the TNA which is immediately
CC adjacent to the complementary region of the first probe. When the probes
CC are bound to the TNA, they can be ligated together using a conventional
CC

CC ligase. The TNA:ligated probe complex can be isolated by binding the
 CC first probe to a paramagnetic bead to which is attached the second half
 CC of the LBP. The TNA can be dissociated from the ligated probe complex
 CC which can then be detected either by a label attached to the second
 CC probe, by using an external probe or by PCR using the ligated probes as a
 CC template. The capture probes AAT09176-7 are used to isolate a region of
 CC the Hepatitis C virus 5' untranslated region. This region can then be
 CC detected by the probes AAT09178-9 to produce the ligated amplification
 CC sequence AAT09180. The ligated sequence can subsequently be detected by
 CC PCR amplification with the primers AAT09181-3

CC Revised record issued on 21-OCT-2004 : Correction to Feature Table Key

XX

SQ Sequence 45 BP; 11 A; 16 C; 12 G; 6 T; 0 U; 0 Other;

Query Match

10.8%; Score 41.4; DB 2; Length 45;

Best Local Similarity 76.7%; Pred. No. 0.022;

Matches 33; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 228 UGGGCGUGCCCCCGGAGACUGCUAGCCGAGUAGUGUGGGUC 270

:||||:||||||| ||||:||||:|||||||:||||:|

Db 45 TGGGCGTGCCCCCGCAAGACTGCTAGCCGAGTAGTGTGGGTC 3

RESULT 15

AAV20718/c

ID AAV20718 standard; DNA; 45 BP.

XX

AC AAV20718;

XX

DT 17-JUL-1998 (first entry)

XX

DE Hepatitis C virus probe SEQ ID NO:23.

vv

XX Hepatitis C virus; HCV; HIV; probe; detection; capture; amplification;
KW paramagnetic particle; ligation; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
PN WO9804745-A1.
XX
PD 05-FEB-1998.
XX
PF 30-JUL-1997; 97WO-US013390.
XX
PR 31-JUL-1996; 96US-00690495.
XX
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Zhang DY, Brandwein M;
XX
DR WPI; 1998-159153/14.
XX
PT Detection of target nucleic acids in samples - using capture and
PT amplification probes, paramagnetic particles and ligation to form a
PT nucleotide sequence which can be detected.
XX
PS Example 4; Page 62; 136pp; English.
XX
CC The present sequence represents a probe used in an example of the present
CC invention for the detection of HCV RNA in a sample. The present invention
CC describes methods for: (A) detecting a target nucleic acid (NA) in a
CC sample; (B) in situ detection of a target NA in a sample; (C) detecting
CC an antigen in a sample; and (D) detecting an antibody in a sample. The
CC methods can be used for the rapid automated detection and monitoring of
CC pathogenic organisms as well as the detection of abnormal levels in an

CC pathogenic organisms, as well as the detection of abnormal genes in an
 CC individual. The methods allow for isolation, amplification and detection
 CC of NA sequences corresponding to the target NA to be carried out in the
 CC same receptacle, e.g. tube or micro-well plate. The method also allows
 CC for standardisation of conditions, because only a pair of generic
 CC amplification probes may be utilised in the present method for detecting
 CC a variety of target NAs, thus allowing efficient multiplex amplification.
 CC The method also allows the direct detection of RNA by probe amplification
 CC without the need for DNA template production. The amplification probes,
 CC which may be covalently joined end to end, form a contiguous ligated
 CC amplification sequence. The assembly of the amplifiable DNA by ligation
 CC increase specificity, and makes possible the detection of a single
 CC mutation in a target

XX

SQ Sequence 45 BP; 11 A; 16 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 10.8%; Score 41.4; DB 2; Length 45;
 Best Local Similarity 76.7%; Pred. No. 0.022;
 Matches 33; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 228 UGGCGUGCCCCCGGAGACUGCUAGCCGAGUAGUGUUGGGUC 270

Db 45 TGGCGGTGCCCCCGCAAGACTGCTAGCCGAGTAGTGTGGGTC 3
 :||||:||||||| ||||:|||||||:||||:||||:|

Search completed: September 21, 2007, 14:29:16
 Job time : 445 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2007, 15:31:59 ; Search time 372 Seconds
(without alignments)
609.417 Million cell updates/sec

Title: US-10-626-879-1
Perfect score: 21
Sequence: 1 guacugccugauaggugcuu 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 8735976

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_200711:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000:*
4: geneseqn2001:*

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4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*
14: geneseqn2004c:*
15: geneseqn2004d:*
16: geneseqn2005a:*
17: geneseqn2005b:*
18: geneseqn2005c:*
19: geneseqn2006a:*
20: geneseqn2006b:*
21: geneseqn2006c:*
22: geneseqn2007:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query Match		Length	DB	ID	Description
	Score	Match				
1	21	100.0	21	12	ADJ38935	Hepatitis
2	21	100.0	21	16	ADY75012	Hepatitis
3	21	100.0	21	16	ADZ02291	Hepatitis
4	21	100.0	21	16	ADZ02349	Hepatitis
5	21	100.0	21	16	ADZ02349	Hepatitis

5	21	100.0	21	16	AEC61919	Aec61919	Hepatitis
6	21	100.0	21	16	AEC61977	Aec61977	Hepatitis
7	21	100.0	21	19	AEg73671	Aeg73671	HCV 5' UT
8	21	100.0	21	19	AEg96040	Aeg96040	Hepatitis
9	21	100.0	21	19	AEI66282	Aei66282	Hepatitis
10	21	100.0	21	19	AEK46630	Aek46630	HCV modif
11	21	100.0	21	19	AEK46688	Aek46688	HCV modif
12	21	100.0	23	10	ADF52816	Adf52816	Hepatitis
13	21	100.0	23	10	ADF52817	Adf52817	Hepatitis
14	21	100.0	23	10	ADF52973	Adf52973	Hepatitis
15	21	100.0	23	10	ADF52915	Adf52915	Hepatitis
16	21	100.0	23	16	ADZ02137	Adz02137	Hepatitis
17	21	100.0	23	16	ADZ02138	Adz02138	Hepatitis
18	21	100.0	23	16	ADZ02173	Adz02173	Hepatitis
19	21	100.0	23	16	AEC61765	Aec61765	Hepatitis
20	21	100.0	23	16	AEC61766	Aec61766	Hepatitis
21	21	100.0	23	16	AEC61801	Aec61801	Hepatitis
22	21	100.0	23	19	AEK46476	Aek46476	HCV targe
23	21	100.0	23	19	AEK46477	Aek46477	HCV targe
24	21	100.0	23	19	AEK46512	Aek46512	HCV targe
25	21	100.0	24	5	AAD19057	Aad19057	Hepatitis
26	21	100.0	27	2	AAT67195	Aat67195	Hepatitis
27	21	100.0	27	3	AZ87367	Aaz87367	Hepatitis
28	21	100.0	27	3	AAA74623	Aaa74623	HCV-speci
29	21	100.0	27	5	AAH78439	Aah78439	PCR prime
30	21	100.0	27	5	AAH78441	Aah78441	PCR prime
31	21	100.0	27	19	AEg73676	Aeg73676	HCV 5' UT
32	21	100.0	27	19	AEI66298	Aei66298	Hepatitis
33	21	100.0	28	2	AAT05222	Aat05222	Hepatitis
34	21	100.0	28	2	AAT67194	Aat67194	Hepatitis
35	21	100.0	28	2	AAV59059	Aav59059	Primer ST
36	21	100.0	28	3	AZ57757	Aaz57757	Hepatitis
37	21	100.0	28	4	AAH25414	Aah25414	Reverse P
38	21	100.0	28	10	AAH25414	Aah25414	Reverse P

C	38	21	100.0	28	10	ADC84693	Adc84693 PCR prime
C	39	21	100.0	28	22	AER42522	Aer42522 HCV RNA a
C	40	21	100.0	28	22	AES98404	Aes98404 Hepatitis
C	41	21	100.0	28	22	AFK91236	Afk91236 Hepatitis
C	42	21	100.0	29	6	AAD43740	Aad43740 HCV DNA a
C	43	21	100.0	29	6	AAD43288	Aad43288 HCV DNA a
C	44	21	100.0	29	9	ADC54073	Adc54073 HCV 5'UTR
C	45	21	100.0	30	2	AAQ55728	Aaq55728 Hepatitis
C	46	21	100.0	30	22	AFY25780	Afy25780 HCV RNA R
C	47	21	100.0	33	2	AAQ31158	Aaq31158 Probe 127
C	48	21	100.0	33	2	AAQ46464	Aaq46464 Hepatitis
C	49	21	100.0	33	2	AAV07838	Aav07838 HCV.33.9
C	50	21	100.0	33	2	AAV83066	Aav83066 Amplifier
C	51	21	100.0	40	2	AAV54436	Aav54436 Nucleotid
	52	20	95.2	21	16	ADZ02350	Adz02350 Hepatitis
	53	20	95.2	21	16	ADZ02292	Adz02292 Hepatitis
	54	20	95.2	21	16	AEC61920	Aec61920 Hepatitis
	55	20	95.2	21	16	AEC61978	Aec61978 Hepatitis
	56	20	95.2	21	19	AEG73674	Aeg73674 HCV 5' UT
	57	20	95.2	21	19	AEI66297	Aei66297 Hepatitis
	58	20	95.2	21	19	AEK46631	Aek46631 HCV modif
	59	20	95.2	21	19	AEK46689	Aek46689 HCV modif
	60	20	95.2	23	10	ADF52916	Adf52916 Hepatitis
	61	20	95.2	23	10	ADF52974	Adf52974 Hepatitis
	62	20	95.2	23	10	ADF52815	Adf52815 Hepatitis
	63	20	95.2	23	10	ADF52818	Adf52818 Hepatitis
	64	20	95.2	23	16	ADZ02136	Adz02136 Hepatitis
	65	20	95.2	23	16	ADZ02139	Adz02139 Hepatitis
	66	20	95.2	23	16	AEC61764	Aec61764 Hepatitis
	67	20	95.2	23	16	AEC61767	Aec61767 Hepatitis
	68	20	95.2	23	19	AEK46475	Aek46475 HCV targe
	69	20	95.2	23	19	AEK46478	Aek46478 HCV targe
	70	20	95.2	25	19	AEG73678	Aeg73678 HCV 5' UT
	71	20	95.2	25	19	AEG73678	Aeg73678 HCV 5' UT

71	20	95.2	25	19	AEI66299	Aei66299 Hepatitis
C 72	20	95.2	27	2	AAQ71839	Aaq71839 PCR prime
C 73	20	95.2	27	3	AAA74624	Aaa74624 HCV-speci
C 74	20	95.2	27	5	ABK09262	Abk09262 Enzymatic
75	20	95.2	27	5	ABK09264	Abk09264 Enzymatic
C 76	20	95.2	27	5	ABA02736	Aba02736 Nucleic a
77	20	95.2	27	5	ABA02738	Aba02738 Nucleic a
78	19	90.5	19	10	ADF51425	Adf51425 Hepatitis
79	19	90.5	19	10	ADF51419	Adf51419 Hepatitis
80	19	90.5	19	10	ADF51426	Adf51426 Hepatitis
C 81	19	90.5	19	10	ADF52115	Adf52115 Hepatitis
C 82	19	90.5	19	10	ADF52121	Adf52121 Hepatitis
C 83	19	90.5	19	10	ADF52122	Adf52122 Hepatitis
C 84	19	90.5	19	16	ADZ01443	Adz01443 Hepatitis
85	19	90.5	19	16	ADZ00746	Adz00746 Hepatitis
86	19	90.5	19	16	ADZ00747	Adz00747 Hepatitis
87	19	90.5	19	16	ADZ00740	Adz00740 Hepatitis
C 88	19	90.5	19	16	ADZ01436	Adz01436 Hepatitis
C 89	19	90.5	19	16	ADZ01442	Adz01442 Hepatitis
90	19	90.5	19	16	AEC60368	Aec60368 Hepatitis
91	19	90.5	19	16	AEC60374	Aec60374 Hepatitis
92	19	90.5	19	16	AEC60375	Aec60375 Hepatitis
C 93	19	90.5	19	16	AEC61064	Aec61064 Hepatitis
C 94	19	90.5	19	16	AEC61070	Aec61070 Hepatitis
C 95	19	90.5	19	16	AEC61071	Aec61071 Hepatitis
96	19	90.5	19	19	AEK45079	Aek45079 HCV targe
97	19	90.5	19	19	AEK45085	Aek45085 HCV targe
98	19	90.5	19	19	AEK45086	Aek45086 HCV targe
C 99	19	90.5	19	19	AEK45775	Aek45775 HCV siRNA
C 100	19	90.5	19	19	AEK45781	Aek45781 HCV siRNA
C 101	19	90.5	19	19	AEK45782	Aek45782 HCV siRNA
C 102	19	90.5	21	5	ABA03376	Aba03376 Human gen
C 103	19	90.5	21	10	ADF52987	Adf52987 Hepatitis
C 104	19	90.5	21	10	ADF52985	Adf52985 Hepatitis

C 104	19	90.5	21	10	ADF52985	Adf52985	Hepatitis
C 105	19	90.5	21	10	ADF52927	Adf52927	Hepatitis
C 106	19	90.5	21	10	ADF52986	Adf52986	Hepatitis
C 107	19	90.5	21	10	ADF52928	Adf52928	Hepatitis
C 108	19	90.5	21	10	ADF52929	Adf52929	Hepatitis
C 109	19	90.5	21	12	ADJ38936	Adj38936	Hepatitis
110	19	90.5	21	13	ADV97471	Adv97471	Hepatitis
111	19	90.5	21	13	ADV97441	Adv97441	Hepatitis
C 112	19	90.5	21	16	ADY75013	Ady75013	Hepatitis
C 113	19	90.5	21	16	ADZ02363	Adz02363	Hepatitis
C 114	19	90.5	21	16	ADZ02565	Adz02565	Hepatitis
115	19	90.5	21	16	ADZ02525	Adz02525	Hepatitis
C 116	19	90.5	21	16	ADZ02304	Adz02304	Hepatitis
C 117	19	90.5	21	16	ADZ02305	Adz02305	Hepatitis
C 118	19	90.5	21	16	ADZ02303	Adz02303	Hepatitis
C 119	19	90.5	21	16	ADZ02361	Adz02361	Hepatitis
C 120	19	90.5	21	16	ADZ02362	Adz02362	Hepatitis
121	19	90.5	21	16	AEC62153	Aec62153	Hepatitis
C 122	19	90.5	21	16	AEC62193	Aec62193	Hepatitis
C 123	19	90.5	21	16	AEC61931	Aec61931	Hepatitis
C 124	19	90.5	21	16	AEC61932	Aec61932	Hepatitis
C 125	19	90.5	21	16	AEC61933	Aec61933	Hepatitis
C 126	19	90.5	21	16	AEC61989	Aec61989	Hepatitis
C 127	19	90.5	21	16	AEC61990	Aec61990	Hepatitis
C 128	19	90.5	21	16	AEC61991	Aec61991	Hepatitis
C 129	19	90.5	21	17	AED25029	Aed25029	Short int
C 130	19	90.5	21	17	AED24897	Aed24897	Short int
C 131	19	90.5	21	19	AEK77228	Aek77228	Hepatitis
C 132	19	90.5	21	19	AEK94843	Aek94843	HCV targe
C 133	19	90.5	21	19	AEK46642	Aek46642	HCV modif
C 134	19	90.5	21	19	AEK46643	Aek46643	HCV modif
C 135	19	90.5	21	19	AEK46644	Aek46644	HCV modif
C 136	19	90.5	21	19	AEK46700	Aek46700	HCV modif
137	19	90.5	21	19	AEK46701	Aek46701	HCV modif

C 137	19	19	90.5	21	19	AEK46701	Aek46701	HCV modif
C 138	19	19	90.5	21	19	AEK46702	Aek46702	HCV modif
139	19	19	90.5	21	19	AEK46864	Aek46864	HCV modif
C 140	19	19	90.5	21	19	AEK46904	Aek46904	HCV modif
C 141	19	19	90.5	21	19	AEK78214	Aek78214	Gene expr
C 142	19	19	90.5	21	19	AEK62155	Aek62155	Exemplary
C 143	19	19	90.5	21	19	AEK69542	Aek69542	HCV antis
C 144	19	19	90.5	21	22	AEM47364	Aem47364	HCVa siRN
C 145	19	19	90.5	21	22	AEM83887	Aem83887	HCV siRNA
C 146	19	19	90.5	21	22	AEM84484	Aem84484	HCV siRNA
C 147	19	19	90.5	21	22	AEM92565	Aem92565	HCV siRNA
C 148	19	19	90.5	21	22	AEM91738	Aem91738	HCV siRNA
C 149	19	19	90.5	22	19	AEF57898	Aef57898	Hepatitis
C 150	19	19	90.5	22	22	AFL01190	Afl01190	Antisense
C 151	19	19	90.5	23	2	AAQ53257	Aaq53257	Hepatitis
152	19	19	90.5	23	10	ADF52814	Adf52814	Hepatitis
153	19	19	90.5	23	10	ADF52819	Adf52819	Hepatitis
154	19	19	90.5	23	16	ADZ02140	Adz02140	Hepatitis
155	19	19	90.5	23	16	ADZ02135	Adz02135	Hepatitis
156	19	19	90.5	23	16	AEC61763	Aec61763	Hepatitis
157	19	19	90.5	23	16	AEC61768	Aec61768	Hepatitis
158	19	19	90.5	23	19	AEK46474	Aek46474	HCV targe
159	19	19	90.5	23	19	AEK46479	Aek46479	HCV targe
C 160	19	19	90.5	24	2	AAQ37586	Aaq37586	HCV conse
161	19	19	90.5	24	2	AAQ43144	Aaq43144	HCV core
C 162	19	19	90.5	24	2	AAQ79963	Aaq79963	Primer KY
C 163	19	19	90.5	24	2	AAT64900	Aat64900	Hepatitis
C 164	19	19	90.5	24	2	AAT87095	Aat87095	HCV gene
C 165	19	19	90.5	24	2	AAT93542	Aat93542	Antisense
C 166	19	19	90.5	24	2	AAV15319	Aav15319	Hepatitis
C 167	19	19	90.5	24	2	AAV18850	Aav18850	Primer KY
C 168	19	19	90.5	24	2	AXX23969	Aax23969	PCR prime
C 169	19	19	90.5	24	2	AXX78452	Aax78452	HCV PCR p
C 170	19	19	90.5	24	2	AXX00700	Aax00700	HCV PCR p

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